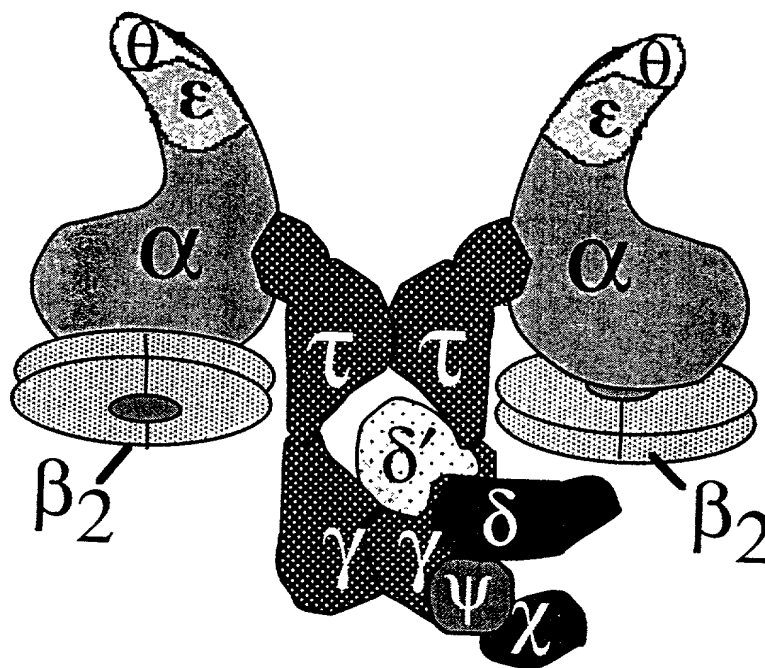


E. coli DNA Polymerase III



Jc882 U.S. PTO
09/642218
08/18/00

Figure 1

ATP binding

E. coli

MSYQVLARKWRPQTFADVVGQEHVLTALANGLSLGRIHHAYLFSGTRGVGKTSIARLLAK

B. subtilis

MSYQALYRVFRPQRFEDVVGQEHITKTLQNALLOKKFSHAYLFSGPRGTGKTSAAKIFAK

**** * * * * * * * * * * . * * * . * * * * * * * * * * * . * *

E. coli

GLNCETGITATPCGVCDNCREIEQGRFVDLIEIDAASRTKVEDTRDLLDNVQYAPARGRF

B. subtilis

AVNCEHAPVDEPCNECAACKGITNGSISDVIEIDAASNNGVDEIRDIRDKVKFAPSAVTY

. * * * * * * * * * * . * * * * * . * * * * * . * * * * * .

E. coli

KVLIDEVHMLSRHSFNALLKTLEEPPEHVKFLLATTPQKLPVTILSRCLQFHLKALDV

B. subtilis

KVYIIDEVHMLSIGAFNALLKTLEEPPEHCIFILATTEPHKIPLTIISRCQRFDFKRITS

* * * * * * * * * * . * * * * * * * * * * . * * * * * * * * * * . * * * * * .

Figure 2

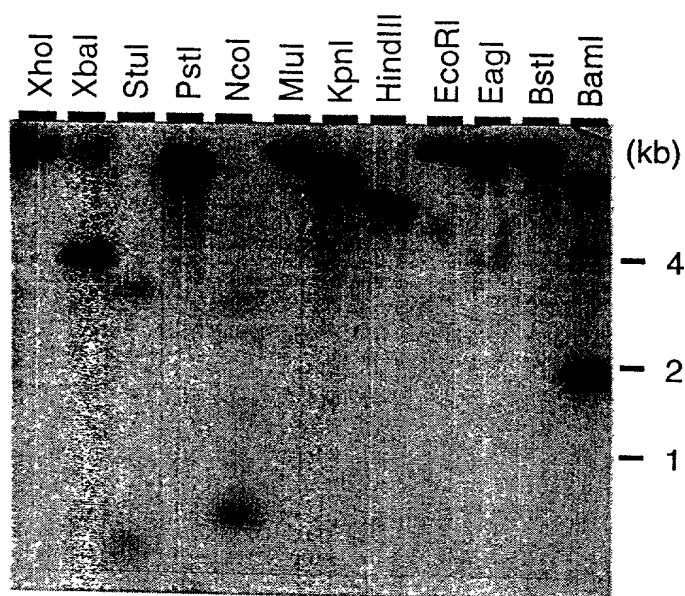


Figure 3

600-1-179 N (Sheet 4 of 31)

| | | | | | | |
|---|---|-------------|------------|------------|--------------------|------------|
| TCCGGGGGTG | GGGTTCCAG | GTAGACCCCG | GCCCCTCCCG | TGAGCCCCTT | TACCCAGGCC | 60 |
| GCCACCTCCT | CCAGGGGGGC | CAAGGCGTGC | AAGGAGAGGA | ACGTCCGCAC | <u>CACGCC</u> CTAT | 120 |
| ACTAGCCTT | GTG AGC GCC CTC TAC CGC CGC TTC CGC CCC CTC ACC TTC CAG GAG GTG GTG | S.D. | | | | 180 |
| | met ser ala leu tyr arg arg phe arg pro leu thr phe gln glu val val | | | | | (17) |
| | | | | | CAC | |
| GGG CAG GAG CAC GTG AAG GAG CCC CTC CTC AAG GCC ATC CGG GAG GGG AGG CTC GCC CAG | gly gln glu his val lys glu pro leu leu lys ala ile arg glu gly arg leu ala gln | | | | | 240 (37) |
| GCS TAC CTS TTC TCC GGS AC | | | | | | |
| GCC TAC CTC TTC TCC GGG CCC AGG GGC GTG GGC AAG ACC ACC ACG GCG AGG CTC CTC GCC | ala tyr leu phe ser gly pro arg gly val gly lys thr thr thr ala arg leu leu ala | | | | | 300 (57) |
| ATG GCG GTG GGG TGC CAG GGG GAA GAC CCC CCT TGC GGG GTC TGC CCC CAC TGC CAG GCG | met ala val gly cys gln gly glu asp pro pro cys gly val cys pro his cys gln ala | | | | | 360 (77) |
| GTG CAG AGG GGC GCC CAC CCG GAC GTG GTG GAC ATT GAC GCC GCC AGC AAC AAC TCC GTG | val gln arg gly ala his pro asp val val asp ile asp ala ala ser asn asn ser val | | | | | 420 (97) |
| GAG GAC GTG CGG GAG CTG AGG GAA AGG ATC CAC CTC GCC CCC CTC TCT GCC CCC AGG AAG | glu asp val arg glu leu arg glu arg ile his leu ala pro leu ser ala pro arg lys | | | | | 480 (117) |
| | | | | | C | |
| GTC TTC ATC CTG GAC GAG GCC CAC ATG CTC TCC AAA AGC GCC TTC AAC GCC CTC CTC AAG | val phe ile leu asp Glu ala his met leu ser lys ser ala phe asn ala leu leu lys | | | | | 540 (137) |
| TGS CTS CTC CTC GGS GGS CTC GTG | | | | | | |
| ACC CTG GAG GAG CCC CCG CCC CAC GTC CTC TTC GTC TTC GCC ACC ACC GAG CCC GAG AGG | thr leu glu glu pro pro pro his val leu phe val phe ala thr thr glu pro glu arg | | | | | 600 (157) |
| ATG CCC CCC ACC ATC CTC TCC CGC ACC CAG CAC TTC CGC TTC CGC CGC CTC ACG GAG GAG | met pro pro thr ile leu ser arg thr gln his phe arg phe arg arg leu thr glu glu | | | | | 660 (177) |
| GAG ATC GCC TTT AAG CTC CGG CGC ATC CTG GAG GCC GTG GGG CGG GAG GCG GAG GAG GAG | glu ile ala phe lys leu arg arg ile leu glu ala val gly arg glu ala glu glu glu | | | | | 720 (197) |
| GCC CTC CTC CTC CTC GCC CGC CTG GCG GAC GGG GCC CTT AGG GAC GCG GAA AGC CTC CTG | ala leu leu leu leu ala arg leu ala asp gly ala leu arg asp ala glu ser leu leu | | | | | 780 (217) |
| GAG CGC TTC CTC CTC CTG GAA GGC CCC CTC ACC CGG AAG GAG GTG GAG CGC GCC CTA GGC | glu arg phe leu leu leu glu gly pro leu thr arg lys glu val glu arg ala leu gly | | | | | 840 (237) |
| TCC CCC CCA GGG ACC GGG GTG GCC GAG ATC GCC GCC TCC CTC GCG AGG GGG AAA ACG GCG | ser pro pro gly thr gly val ala glu ile ala ala ser leu ala arg gly lys thr ala | | | | | 900 (257) |
| GAG GCC CTG GGC CTC GCC CGG CGC CTC TAC GGG GAA GGG TAC GCC CCG AGG AGC CTG GTC | glu ala leu gly leu ala arg arg leu tyr gly glu gly tyr ala pro arg ser leu val | | | | | 960 (277) |
| TCG GGC CTT TTG GAG GTG TTC CGG GAA GGC CTC TAC GCC GCC TTC GGC CTC GCG GGA ACC | ser gly leu leu glu val phe arg glu gly leu tyr ala ala phe gly leu ala gly thr | | | | | 1020 (297) |
| CCC CTT CCC GCC CCG CCC CAG GCC CTG ATC GCC GCC ATG ACC GCC CTG GAC GAG GCC ATG | pro leu pro ala pro pro gln ala leu ile ala ala met thr ala leu asp glu ala met | | | | | 1080 (317) |

Figure 4A

| | |
|---|-------|
| GAG CGC CTC GCC CGC CGC TCC GAC GCC TTA AGC CTG GAG GTG GCC CTC CTG GAG GCG GGA | 1140 |
| glu arg leu ala arg arg ser asp ala leu ser leu glu val ala leu leu glu ala gly | (337) |
| AGG GCC CTG GCC GCC GAG GCC CTA CCC CAG CCC ACG GGC GCT CCT TCC CCA GAG GTC GGC | 1200 |
| arg ala leu ala ala glu ala leu pro gln pro thr gly ala pro ser pro glu val gly | (357) |
| CCC AAG CCG GAA AGC CCC CCG ACC CCG GAA CCC CCA AGG CCC GAG GAG GCG CCC GAC CTG | 1260 |
| pro lys pro glu ser pro pro thr pro glu pro pro arg pro glu glu ala pro asp leu | (377) |
| CGG GAG CGG TGG CGG GCC TTC CTC GAG GCC CTC AGG CCC ACC CTA CGG GCC TTC GTG CGG | 1320 |
| arg glu arg trp arg ala phe leu glu ala leu arg pro thr leu arg ala phe val arg | (397) |
| GAG GCC CGC CCG GAG GTC CGG GAA GGC CAG CTC TGC CTC GCT TTC CCC GAG GAC AAG GCC | 1380 |
| glu ala arg pro glu val arg glu gly gln leu cys leu ala phe pro glu asp lys ala | (417) |
| TTC CAC TAC CGC AAG GCC TCG GAA CAG AAG GTG AGG CTC CTC CCC CTG GCC CAG GCC CAT | 1440 |
| phe his tyr arg lys ala ser glu gln lys val arg leu leu pro leu ala gln ala his | (437) |
| frameshift site | |
| TTC GGG GTG GAG GAG GTC GTC CTC GTC CTG GAG GGA GAA AAA AAA AGC CTG AGC CCA AGG | 1500 |
| phe gly val glu glu val val leu val leu glu gly glu lys lys ser leu ser pro arg | (457) |
| CCC CGC CCG GCC CCA CCT CCT GAA GCG CCC GCA CCC CCG GGC CCT CCC GAG GAG GAG GTA | 1560 |
| pro arg pro ala pro pro pro glu ala pro ala pro pro gly pro pro glu glu glu val | (477) |
| GAG GCG GAG GAA GCG GCG GAG GAG GCC CCG GAG GAG GCC TTG AGG CGG GTG GTC CGC CTC | 1620 |
| glu ala glu glu ala ala glu glu ala pro glu glu ala leu arg arg val val arg leu | (497) |
| CTG GGG GGG CGG GTG CTC TGG GTG CGG CGG CCC AGG ACC CGG GAG GCG CCG GAG GAG GAA | 1680 |
| leu gly gly arg val leu trp val arg arg pro arg thr arg glu ala pro glu glu glu | (517) |
| CCC CTG AGC CAA GAC GAG ATA GGG GGT ACT GGT ATA TAA TGGGGGCATG ACGCGGACCAC | 1740 |
| pro leu ser gln asp glu ile gly gly thr gly ile * | (529) |
| CGACCTCGGA CAAGAGACCG TGGACAACAT CCTCAAGCGC CTCCGCCGTA TTGAGGGCCA | 1820 |
| GGTGCGGGGG CTCCAGAAGA TGGTGGCCGA GGGCCGCCCC TGCGACGAGG TCCTCACCAC | 1880 |
| GATGACCGCC ACCAAGAAGG CCATGGAGGC GGCGGCCACC CTGATCCTCC ACGAGTTCCT | 1940 |
| GAACGTCTGC GCCGCCGAGG TCTCCGAGGG CAAGGTGAAC CCCAAGAAGC CCGAGGAGAT | 2000 |
| CGCCACCATG CTGAAGAAGT TCATCTA | 2027 |

Figure 4B

| | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--------|-----|-----|------|------|
| | | | GTG | AGC | GCC | CTC | TAC | CGC | CGC | TTC | CGC | CCC | CTC | ACC | TTC | CAG | GAG | GTG | GTG | 51 |
| GGG | CAG | GAG | CAC | GTG | AAG | GAG | CCC | CTC | CTC | AAG | GCC | ATC | CGG | GAG | GGG | AGG | CTC | GCC | CAG | 111 |
| GCC | TAC | CTC | TTC | TCC | GGG | CCC | AGG | GGC | GTG | GGC | AAG | ACC | ACC | ACG | GCG | AGG | CTC | CTC | GCC | 171 |
| ATG | GCG | GTG | GGG | TGC | CAG | GGG | GAA | GAC | CCC | CCT | TGC | GGG | GTC | TGC | CCC | CAC | TGC | CAG | GCG | 231 |
| GtG | CAG | AGG | GGC | GCC | CAC | CCG | GAC | GTG | GTG | GAC | ATT | GAC | GCC | GCC | AGC | AAC | AAC | TCC | GTG | 291 |
| GAG | GAC | GTG | CGG | GAG | CTG | AGG | GAA | AGG | ATC | CAC | CTC | GCC | CCC | CTC | TCT | GCC | CCC | AGG | AAG | 351 |
| GTC | TTC | ATC | CTG | GAC | GAG | GCC | CAC | ATG | CTC | TCC | AAA | AGC | GCC | TTC | AAC | GCC | CTC | CTC | AAG | 411 |
| ACC | CTG | GAG | GAG | CCC | CCG | CCC | CAC | GTC | CTC | TTC | GTC | TTC | GCC | ACC | ACC | GAG | CCC | GAG | AGG | 471 |
| ATG | CCC | CCC | ACC | ATC | CTC | TCC | CGC | ACC | CAG | CAC | TTC | CGC | TTC | CGC | CGC | CTC | ACG | GAG | GAG | 531 |
| GAG | ATC | GCC | TTT | AAG | CTC | CGG | CGC | ATC | CTG | GAG | GCC | GTG | GGG | CGG | GAG | GCG | GAG | GAG | GAG | 591 |
| GCC | CTC | CTC | CTC | CTC | GCC | CGC | CTG | GCG | GAC | GGG | GCC | CTT | AGG | GAC | GCG | GAA | AGC | CTC | CTG | 651 |
| GAG | CGC | TTC | CTC | CTC | CTG | GAA | GGC | CCC | CTC | ACC | CGG | AAG | GAG | GTG | GAG | CGC | GCC | CTA | GGC | 711 |
| TCC | CCC | CCA | GGG | ACC | GGG | GTG | GCC | GAG | ATC | GCC | GCC | TCC | CTC | GCG | AGG | GGG | AAA | ACG | GCG | 771 |
| GAG | GCC | CTG | GGC | CTC | GCC | CGG | CGC | CTC | TAC | GGG | GAA | GGG | TAC | GCC | CCG | AGG | AGC | CTG | GTC | 831 |
| TCG | GGC | CTT | TTG | GAG | GTG | TTC | CGG | GAA | GGC | CTC | TAC | GCC | GCC | TTC | GGC | CTC | GCG | GGA | ACC | 891 |
| CCC | CTT | CCC | GCC | CCG | CCC | CAG | GCC | CTG | ATC | GCC | GCC | ATG | ACC | GCC | CTG | GAC | GAG | GCC | ATG | 951 |
| GAG | CGC | CTC | GCC | CGC | CGC | TCC | GAC | GCC | TTA | AGC | CTG | GAG | GTG | GCC | CTC | CTG | GAG | CCG | GGA | 1011 |
| AGG | GCC | CTG | GCC | GCC | GAG | GCC | CTA | CCC | CAG | CCC | ACG | GGC | GCT | CCT | TCC | CCA | GAG | GTC | GGC | 1071 |
| CCC | AAG | CCG | GAA | AGC | CCC | CCG | ACC | CCG | GAA | CCC | CCA | AGG | CCC | GAG | GAG | GCG | CCC | GAC | CTG | 1131 |
| CGG | GAG | CGG | TGG | CGG | GCC | TTC | CTC | GAG | GCC | CTC | AGG | CCC | ACC | CTA | CGG | GCC | TTC | GTG | CGG | 1191 |
| GAG | GCC | CGC | CCG | GAG | GTC | CGG | GAA | GGC | CAG | CTC | TGC | CTC | GCT | TTC | CCC | GAG | GAC | AAG | GCC | 1251 |
| TTC | CAC | TAC | CGC | AAG | GCC | TCG | GAA | CAG | AAG | GTG | AGG | CTC | CTC | CCC | CTG | GCC | CAG | GCC | CAT | 1311 |
| TTC | GGG | GTG | GAG | GAG | GTC | GTC | CTC | GTC | CTG | GAG | GGA | GAA | AAA | AAA | AGC | CTG | AGC | CCA | AGG | 1371 |
| CCC | CGC | CCG | GCC | CCA | CCT | GAT | GAA | GCG | CCC | GCA | CCC | CCG | GGC | CCT | CCC | GAG | GAG | GAG | GTA | 1431 |
| GAG | GCG | GAG | GAA | GCG | GCG | GAG | GAG | GCC | CCG | GAG | GAG | GCC | TTG | AGG | CGG | GTG | GTC | CGC | CTC | 1491 |
| CTG | GGG | GGG | CGG | GTG | CTC | TGG | GTG | CGG | CGG | CCC | AGG | ACC | CGG | GAG | GCG | CCG | GAG | GAA | 1551 | |
| | | | CCC | CTG | AGC | CAA | GAC | GAG | ATA | GGG | GGT | ACT | GGT | ATA | TAA | (1590) | | | | |

Figure 4C

Met ser ala leu tyr arg arg phe arg pro leu thr phe gln glu val val gly gln glu 20
 his val lys glu pro leu leu lys ala ile arg glu gly arg leu ala gln ala tyr leu 40
 phe ser gly pro arg gly val gly lys thr thr thr ala arg leu leu ala met ala val 60
 gly cys gln gly glu asp pro pro cys gly val cys pro his cys gln ala val gln arg 80
 gly ala his pro asp val val asp ile asp ala ala ser asn asn ser val glu asp val 100
 arg glu leu arg glu arg ile his leu ala pro leu ser ala pro arg lys val phe ile 120
 leu asp glu ala his met leu ser lys ser ala phe asn ala leu leu lys thr leu glu 140
 glu pro pro pro his val leu phe val phe ala thr thr glu pro glu arg met pro pro 160
 thr ile leu ser arg thr gln his phe arg phe arg arg leu thr glu glu glu ile ala 180
 phe lys leu arg arg ile leu glu ala val gly arg glu ala glu glu glu ala leu leu 200
 leu leu ala arg leu ala asp gly ala leu arg asp ala glu ser leu leu glu arg phe 220
 leu leu leu glu gly pro leu thr arg lys glu val glu arg ala leu gly ser pro pro 240
 gly thr gly val ala glu ile ala ala ser leu ala arg gly lys thr ala glu ala leu 260
 gly leu ala arg arg leu tyr gly glu gly tyr ala pro arg ser leu val ser gly leu 280
 leu glu val phe arg glu gly leu tyr ala ala phe gly leu ala gly thr pro leu pro 300
 ala pro pro gln ala leu ile ala ala met thr ala leu asp glu ala met glu arg leu 320
 ala arg arg ser asp ala leu ser leu glu val ala leu leu glu ala gly arg ala leu 340
 ala ala glu ala leu pro gln pro thr gly ala pro ser pro glu val gly pro lys pro 360
 glu ser pro pro thr pro glu pro pro arg pro glu glu ala pro asp leu arg glu arg 380
 trp arg ala phe leu glu ala leu arg pro thr leu arg ala phe val arg glu ala arg 400
 pro glu val arg glu gly gln leu cys leu ala phe pro glu asp lys ala phe his tyr 420
 arg lys ala ser glu gln lys val arg leu leu pro leu ala gln ala his phe gly val 440
 glu glu val val leu val leu glu gly glu lys lys ser leu ser pro arg pro arg pro 460
 ala pro pro pro glu ala pro ala pro pro gly pro pro glu glu glu val glu ala glu 480
 glu ala ala glu glu ala pro glu glu ala leu arg arg val val arg leu leu gly gly 500
 arg val leu trp val arg arg pro arg thr arg glu ala pro glu glu glu pro leu ser 520
 gln asp glu ile gly gly thr gly ile 529

Figure 4D

Met ser ala leu tyr arg arg phe arg pro leu thr phe gln glu val val gly gln glu 20
 his val lys glu pro leu leu lys ala ile arg glu gly arg leu ala gln ala tyr leu 40
 phe ser gly pro arg gly val gly lys thr thr thr ala arg leu leu ala met ala val 60
 gly cys gln gly glu asp pro pro cys gly val cys pro his cys gln ala val gln arg 80
 gly ala his pro asp val val asp ile asp ala ala ser asn asn ser val glu asp val 100
 arg glu leu arg glu arg ile his leu ala pro leu ser ala pro arg lys val phe ile 120
 leu asp glu ala his met leu ser lys ser ala phe asn ala leu leu lys thr leu glu 140
 glu pro pro pro his val leu phe val phe ala thr thr glu pro glu arg met pro pro 160
 thr ile leu ser arg thr gln his phe arg phe arg arg leu thr glu glu glu ile ala 180
 phe lys leu arg arg ile leu glu ala val gly arg glu ala glu glu glu ala leu leu 200
 leu leu ala arg leu ala asp gly ala leu arg asp ala glu ser leu leu glu arg phe 220
 leu leu leu glu gly pro leu thr arg lys glu val glu arg ala leu gly ser pro pro 240
 gly thr gly val ala glu ile ala ala ser leu ala arg gly lys thr ala glu ala leu 260
 gly leu ala arg arg leu tyr gly glu gly tyr ala pro arg ser leu val ser gly leu 280
 leu glu val phe arg glu gly leu tyr ala ala phe gly leu ala gly thr pro leu pro 300
 ala pro pro gln ala leu ile ala ala met thr ala leu asp glu ala met glu arg leu 320
 ala arg arg ser asp ala leu ser leu glu val ala leu leu glu ala gly arg ala leu 340
 ala ala glu ala leu pro gln pro thr gly ala pro ser pro glu val gly pro lys pro 360
 glu ser pro pro thr pro glu pro pro arg pro glu glu ala pro asp leu arg glu arg 380
 trp arg ala phe leu glu ala leu arg pro thr leu arg ala phe val arg glu ala arg 400
 pro glu val arg glu gly gln leu cys leu ala phe pro glu asp lys ala phe his tyr 420
 arg lys ala ser glu gln lys val arg leu leu pro leu ala gln ala his phe gly val 440
 glu glu val val leu val leu glu gly glu lys lys lys pro asp pro lys ala pro pro 460
 gly pro thr ser 464

Figure 4E


```

Met ser ala leu tyr arg arg phe arg pro leu thr phe gln glu val val gly gln glu 20
his val lys glu pro leu leu lys ala ile arg glu gly arg leu ala gln ala tyr leu 40
phe ser gly pro arg gly val gly lys thr thr thr ala arg leu leu ala met ala val 60
gly cys gln gly glu asp pro pro cys gly val cys pro his cys gln ala val gln arg 80
gly ala his pro asp val val asp ile asp ala ala ser asn asn ser val glu asp val 100
arg glu leu arg glu arg ile his leu ala pro leu ser ala pro arg lys val phe ile 120
leu asp glu ala his met leu ser lys ser ala phe asn ala leu leu lys thr leu glu 140
glu pro pro pro his val leu phe val phe ala thr thr glu pro glu arg met pro pro 160
thr ile leu ser arg thr gln his phe arg phe arg arg leu thr glu glu glu ile ala 180
phe lys leu arg arg ile leu glu ala val gly arg glu ala glu glu glu ala leu leu 200
leu leu ala arg leu ala asp gly ala leu arg asp ala glu ser leu leu glu arg phe 220
leu leu leu glu gly pro leu thr arg lys glu val glu arg ala leu gly ser pro pro 240
gly thr gly val ala glu ile ala ala ser leu ala arg gly lys thr ala glu ala leu 260
gly leu ala arg arg leu tyr gly glu gly tyr ala pro arg ser leu val ser gly leu 280
leu glu val phe arg glu gly leu tyr ala ala phe gly leu ala gly thr pro leu pro 300
ala pro pro gln ala leu ile ala ala met thr ala leu asp glu ala met glu arg leu 320
ala arg arg ser asp ala leu ser leu glu val ala leu leu glu ala gly arg ala leu 340
ala ala glu ala leu pro gln pro thr gly ala pro ser pro glu val gly pro lys pro 360
glu ser pro pro thr pro glu pro pro arg pro glu glu ala pro asp leu arg glu arg 380
trp arg ala phe leu glu ala leu arg pro thr leu arg ala phe val arg glu ala arg 400
pro glu val arg glu gly gln leu cys leu ala phe pro glu asp lys ala phe his tyr 420
arg lys ala ser glu gln lys val arg leu leu pro leu ala gln ala his phe gly val 440
glu glu val val leu val leu glu gly glu lys lys lys ala 454

```

Figure 4F

| | | ATP site | |
|---------|---|---------------------------|-----|
| E.coli | MSYQVLARKWRPQTFADVVGQEHVLTALANGLSLGRIHHAYLFS | <u>SGTRGVGKT</u> SIARLLAK | 60 |
| H.inf. |K.....II.....KDN.L..... | F.. | 60 |
| B.sub. |A.Y.VF...R.E.....ITKT.Q.A.LQKKFS..... | P..T....A.KIF.. | 60 |
| C.cres. | DA.T....Y..R..E.LI...AMVRT...AF.T...A..FMLT.V..... | TT.....R | 113 |
| M.gen. | -MH..FYQ.Y..IN.KQTL...SIRKI.V.AINRDKLPNG.I...E..T...TF.KII.. | | 59 |
| T.th. | --VSA.Y.RF..L..QE.....KEP.LKAIRE..LAQ.....P.....TT..... | M | 58 |
| | Zn ⁺⁺ finger | | |
| | * * * * | | |
| E.coli | GLNCET----GITATPCGVCDNCREIEQGRFVDLIEIDAASRTKVEDTRDLLDNVQYAPA | | 116 |
| H.inf. |VH----.V.....E.E..KA....N.I..... | E.....K.V | 116 |
| B.sub. | AV...H---APVDE..NE.AA.KG.TN.SIS.V..... | NNG.DEI..IR.K.KF..S | 116 |
| C.cres. | A..Y..DTVK.PSVDLTTEGYH..S.IE..HM.VL.L..... | DEM.E...G.R...V | 173 |
| M.gen. | AI..LN---WDQIDV.NS..V.KS.NTNSAI.IV..... | KNGIN.I.E.VE..FNH.F | 115 |
| T.th. | AVG.QG-----EDP.....PH.QAVQR.AHP.VVD..... | NNS...V.E.RERHL..L | 112 |
| E.coli | RGRFKVYLIDEVHMLSRHSFNALLKLTLEEPPEHVKFLLATTPQKLPVTILSRCLQFHLK | | 176 |
| H.inf. | V..... | Y..... | 176 |
| B.sub. | AVTY...I.....IGA.....CI.I....E.H.I.L..I...QR.DF. | | 176 |
| C.cres. | EA.Y...I.....TAA.....P.A..IF...EIR.V..... | QR.D.R | 233 |
| M.gen. | TFKK...IL..A...TTQ.WGG.....S.PY.L.IFT...EFN.I.L..... | QS.FF. | 175 |
| T.th. | SAPR..FIL..A....KSA.....P..L.VF...E.ERM.P..... | TQH.RFR | 172 |
| E.coli | ALDVEQIRHQLEHILNEEHIAHEPRALQLLARAAEGSLRDALSLTDQAIASGDGQ--VST | | 234 |
| H.inf. | ...ET..SQH.A...TQ.N.PF.DP..VK..K..Q..I..S..... | M..R.--.TN | 234 |
| B.sub. | RITSQA.VGRMNK.VDA.QLQV.EGS.EII.S..H.GM..... | L....SFSGDI--LKV | 234 |
| C.cres. | RVEPDVLVKHFDR.SAK.GARI.MD..A.I.....V..G...L.... | VQTERGQT.TS | 293 |
| M.gen. | KITSDL.LER.ND.AKK.K.KI.KD..IKI.DLSQ.....G...L..LAI.LIVKKL.LL | | 235 |
| T.th. | R.TE.E.AFK.RR..EAVGREA.EE..L....L.D.A....E..LERFLLLEGP---LTR | | 229 |
| E.coli | QAVSAMLGTLDDDDQALSLVEAMVEANGERVMALINEAAARGIEWEALLVEMLGLLHRIAM | | 294 |
| H.inf. | NV..N...L...NYSVDILY.LHQG...LL.RTLQRV.DAAGD.DK..G.CAEK..Q..L | | 294 |
| B.sub. | EDALLIT.AVSQLYIGK.AKSLHDK.VSDALETL..LLQQ.KDPAK.IED.IFYFRDMLL | | 294 |
| C.cres. | TV.RD...LA.RS.TIA.Y.HVMAGKTKDALEGFRALWGF.ADPVVMLDV.DHC.AS.V | | 353 |
| M.gen. | MLKKHLISLIEMQNL.L.KQFYQ.I | | 260 |
| T.th. | KE.ERA..SPPGTGVAEIAASLARGKTAELG.ARRLYGE.YAPRS.VSGL.EVFREGLY | | 289 |

Figure 5

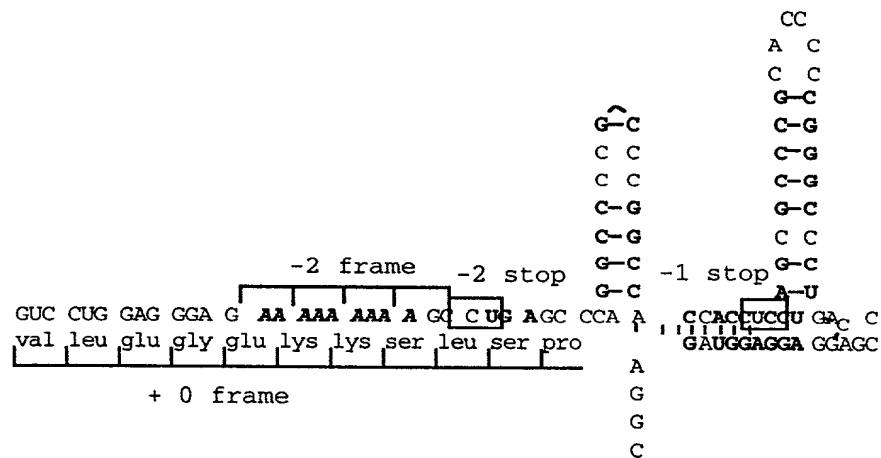


Figure 6

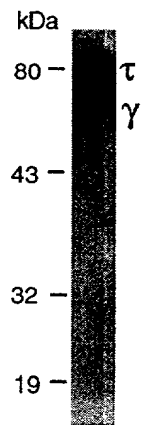
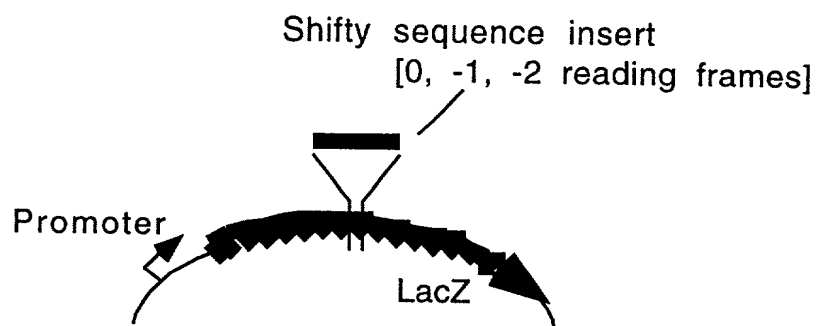


Figure 7



| | Reading
frame | Blue | White |
|-----------------|------------------|------|-------|
| Shifty sequence | 0 | + | |
| | - 1 | + | |
| | - 2 | + | |
| Mutant sequence | 0 | ++ | |
| | - 1 | | + |
| | - 2 | | + |

Figure 8

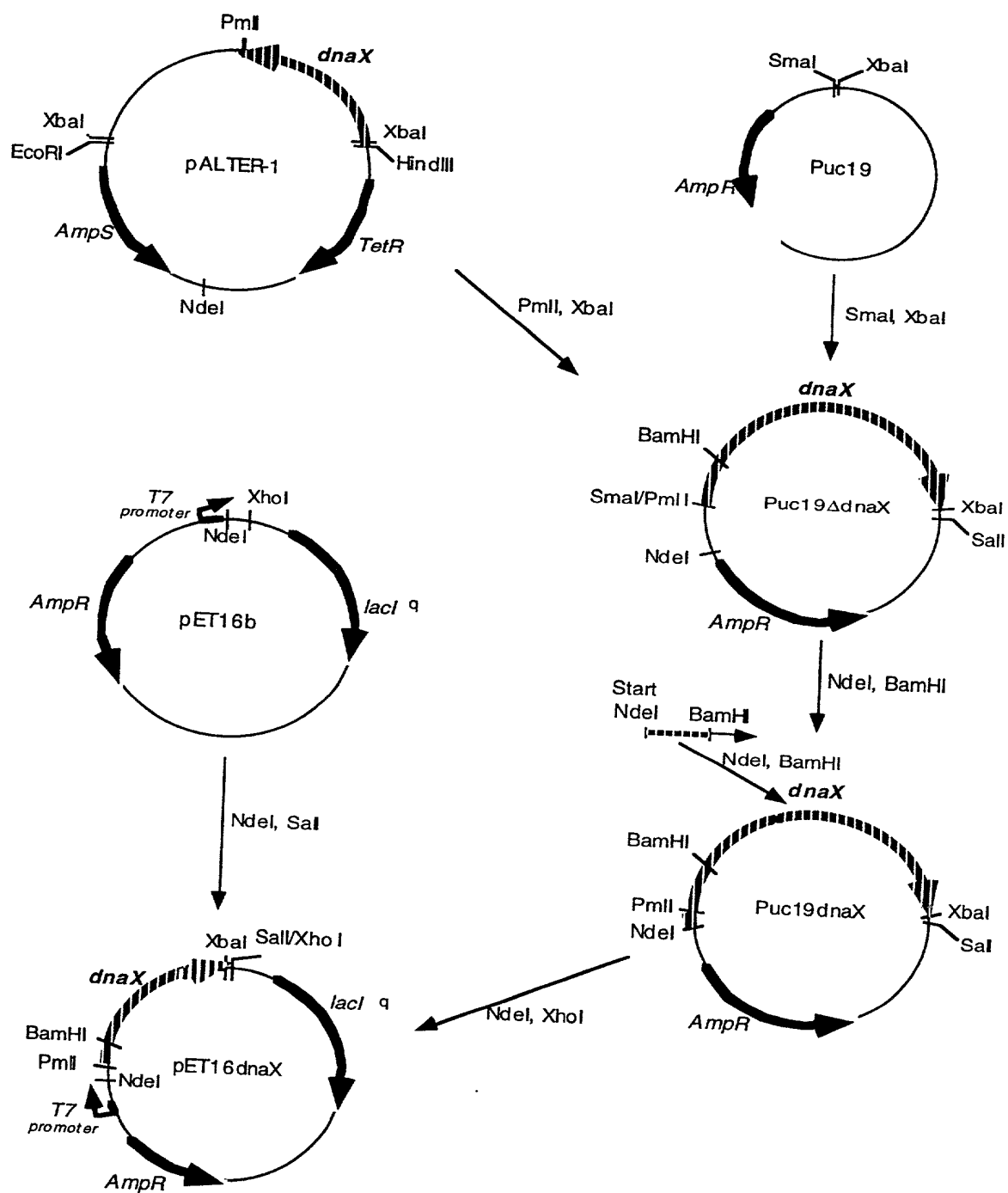


Figure 9

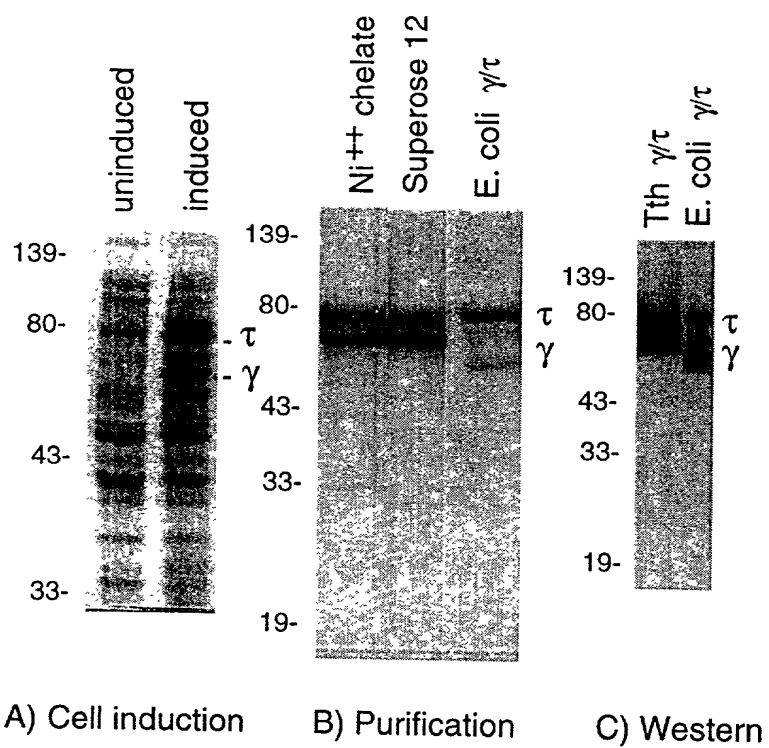


Figure 10

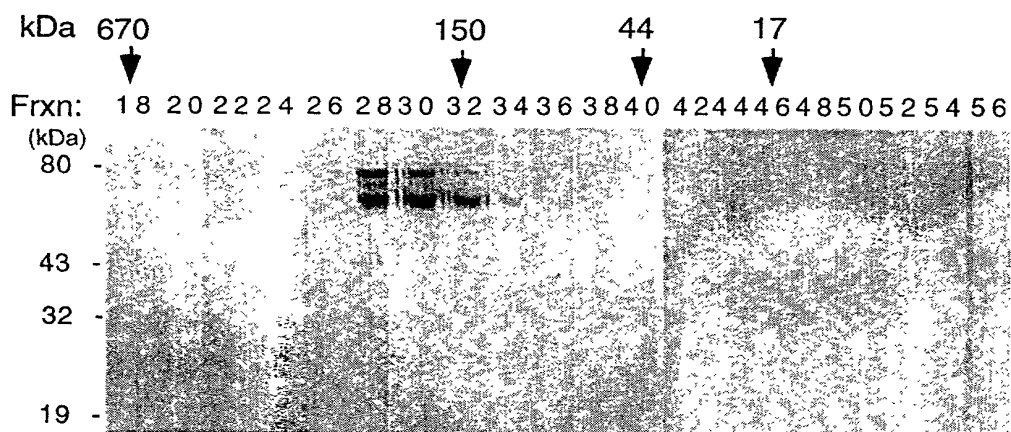
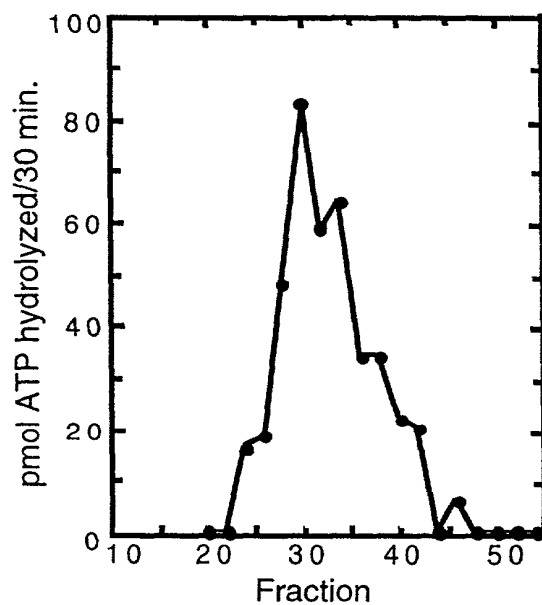


Figure 11

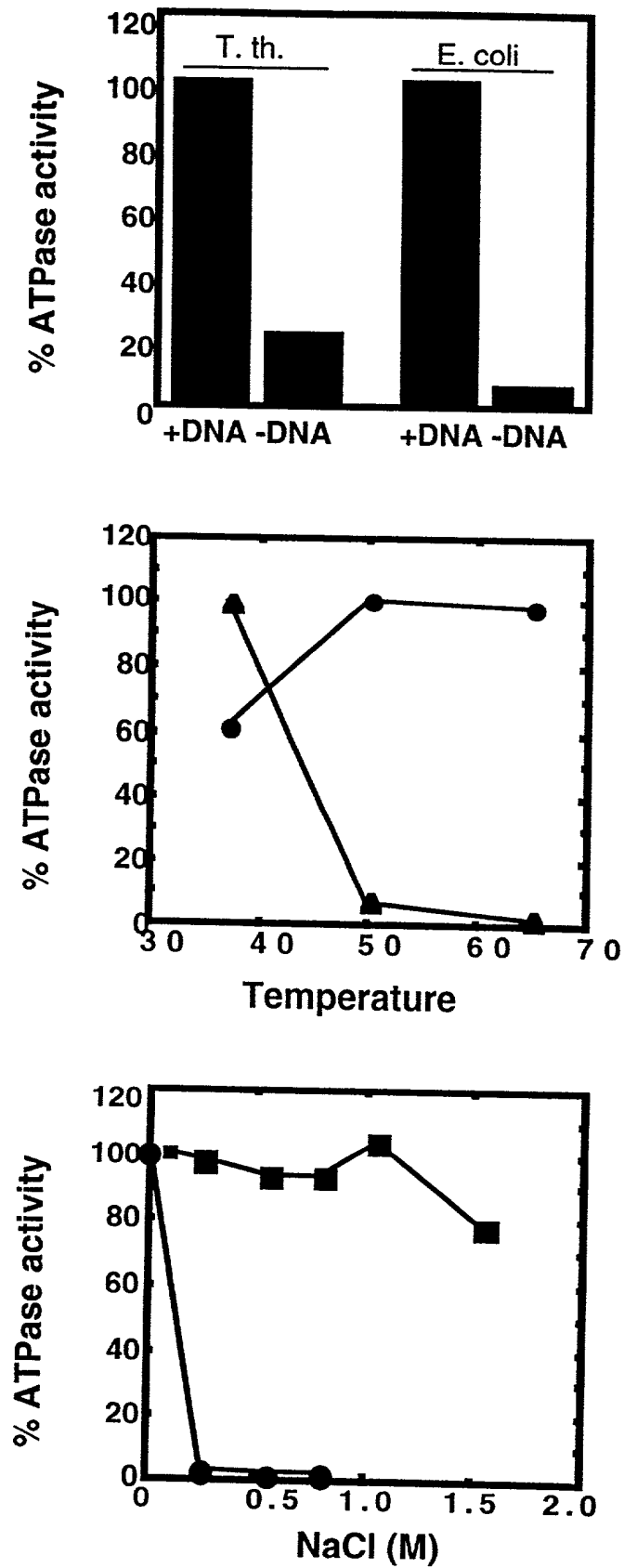
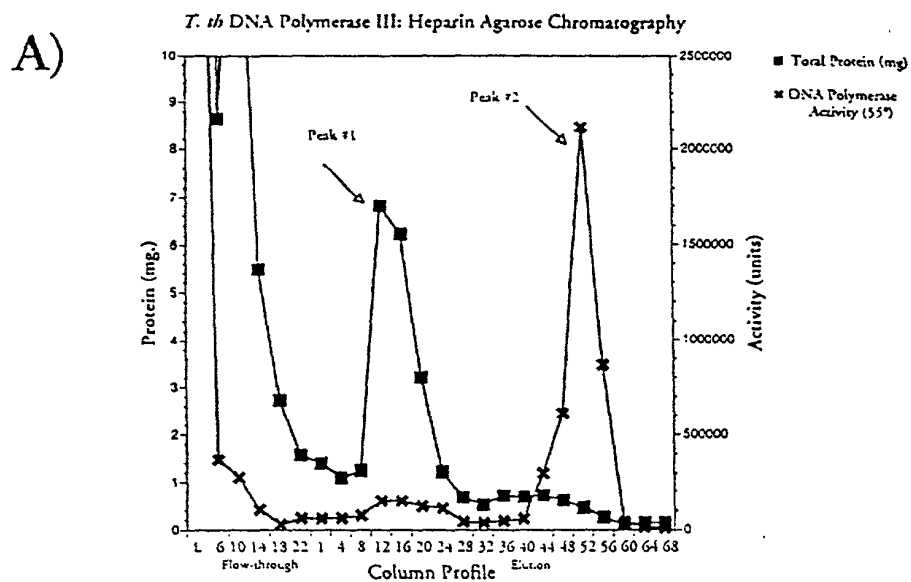


Figure 12



B) ATP Agarose Step Column

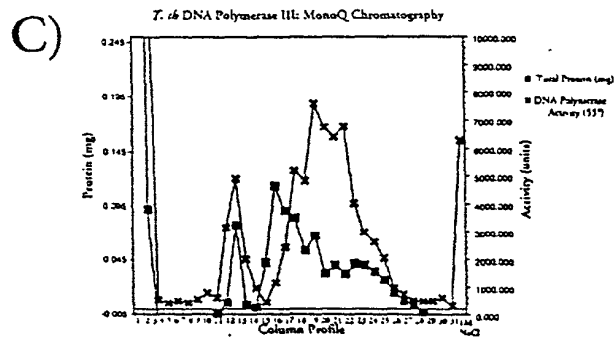
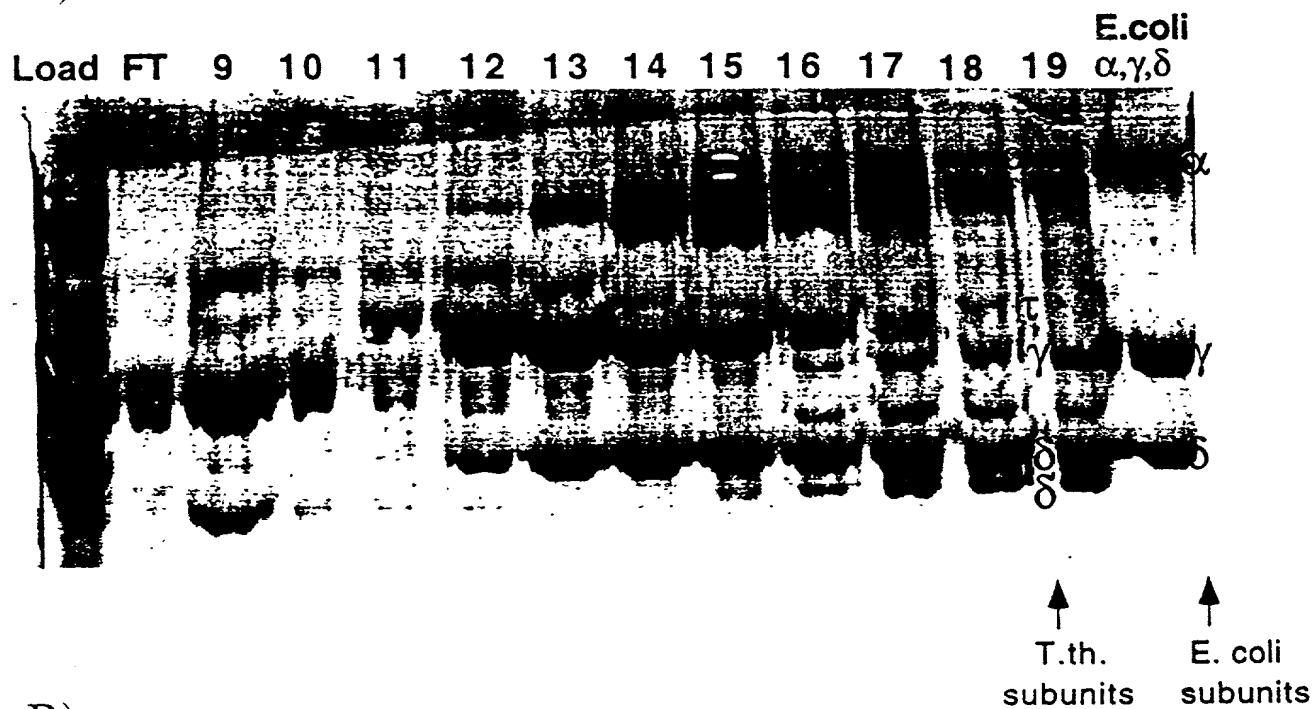


Figure 13

A)



B)

L FT 9 10 11 12 13 14 15 16 17 18 19



Figure 14

A) Alignment of TTH1 with alphas subunits of other organisms.

| | | | |
|---------|------------------------------------|-----|---------|
| E.coli | DRYFLELIRTGRPDEESYLHAAVELAEARGLPVV | 197 | (ID#72) |
| V.chol. | DHFYLELIRTGRADEESYLHFALDVAEQYDLPVV | 197 | (ID#73) |
| H.inf. | DHFYLALSRTGRPNEERYIQAALKLAERCDLPLV | 197 | (ID#74) |
| R.prow. | DRFYFEIMRHDLPEEQFIENSYIQIASELSIPIV | 195 | (ID#75) |
| H.pyl. | DDFYLEIMRHGILDQRFIDEQVIKMSLETGLKII | 213 | (ID#76) |
| S.sp. | DDYYLEIQDHGSVEDRLVNINLVKIAQELDIKIV | 202 | (ID#77) |
| M.tub. | DNYFLELMDHGLTIERRVRDGLLEIGRALNIPPL | 220 | (ID#78) |
| T.th. | FFIEIQNHGLSEQK | | (ID#61) |

B) Alignment of TTH2 with alphas subunits of other organisms.

| | | | |
|---------|--|-----|---------|
| E.coli | NKRRAKNGEPPLDIAAIPLDDKKSFDMLQRSETTAVFQLESRGMKD | 618 | (ID#79) |
| V.chol. | NPRLKKAGKPPVRIEAIPLDDARSFRNLQDAKTTAVFQLESRGMKE | 618 | (ID#80) |
| H.inf. | NVRMVREGKPRVDIAAIPLDDPESFELLKRSETTAVFQLESRGMKD | 618 | (ID#81) |
| R.prow. | CKKLLKEQGIKIDFDDMTFDDKKTQMLCKGKGVGVFQFESIGMKD | 624 | (ID#82) |
| H.pyl. | LKIIKTQHKISVDFLSLDMDDPKVYKTIQSGDTVGIQIES-GMFQ | 648 | (ID#83) |
| S.sp. | QERKALQIRARTGSKKL PDDVKKTHKLEAGDLEGIFQLESQGMKQ | 643 | (ID#84) |
| M.tub. | IDNVRANRGIDLDESVP LDDKATYELLGRGDTLGVFQLDGGPMRD | 646 | (ID#85) |
| T.th. | RVELDYDALTLDD | | (ID#60) |

Figure 15

A)

Start codon

ATGGGCCGGGAGCTCCGCTTCGCCCACCTCCACCAGCACA
 CCCAGTTCTCCCTCCTGGACGGGGCGCCGAAGCTTTCCGA
 CCTCTCAAGTGGGTGGAGGAGACGACCCCGAGGACCCC 120
 GCCTTGGCCATGACCGACCACGGCAACCTCTTCGGGGCCG
 TAGAGTTCTACAAGAAGGCCGCCGAAATGGGCATCGAGCC
 CATCCTGGGTACGAGGCCCTTACGTGGCGGCGGAAAGCCCG 240
 TTTGACCGCAAGCGGGGAAAGGGCCTAGACGGGGGCTACT
 TTCACCTCACCTCCTCGCCAAGGACTTCACGGGGTACCA
 GAACCTGGTGCGCCCTGGCGAGCCGGGCTTACCTGGAGGGG 360
 TTTTACGAAAAGCCCCGGATTGACCGGGAGATCCTGCGCG
 AGCGCCGAGGGCCTCATCGCCTCTCGGGGTGCCTCGGGGC
 GGAGATCCCCCAGTTTCATCCTCCAGGACCGTCTGGACCTG 480
 GCGGAGGCCCCGGCTCAACGAGGACCTCTCCATCTTCAAGG
 ACCGCTTCTTCATTACATCCAGAACCACGGCCTCCCCGA
 GCAGAAAAAGGTCAACGAGGTCTCAAGGAGTTCGCCCCGA 600
 AAGTACGGCCTGGGGATGGTGGCCACCAACGACGGCCATT
 ACGGGAGGAAGGAGGCCCGCAGCGCCACGAGGTTTTCCT
 CGCCATCCAGTCCAAGAGCACCTTGGACGACCCCGGGGCC 720
 GTTGGCTTTCCCTGCGGGAGTTCTACGTGAAGACCCCCG
 AGGAGACGTGCGGGCCGGTGTTCCTCCGAGGAGGAGTGGGG
 GGACGAGCCCTTTGACAACACCGTGGAGATCGCCCGCATG 840
 TGCAACGTGGAGCTGCCCATCGGGACAAGATGGTCTACCC
 GAATCCCCCGCTTCCCCCTCCCCGAGGGACCGGGGACCGA
 GGCCAAGTACCTAATGGAGCTAACCTTCAAGGGGCCCTC 960
 CGCCGTTACCCGGACCGAATCACCGAGGGTTTCTACCGGG
 AGGTTTTCCGCCTTTTGGGGAAGCTTCCCCCCCCACGGGCA
 CGGGGAGGCCTTGGCCGAGGCCTTGGCCCAGGTGGAGCGG 1080
 GAGGCTTGGGAGAGGCTCATGAAGAGCCTCCCCCCTTG
 ACCGGGGTCCAAGGAGTTCCA

B)

MGRELRFALHQHTQFSLLDGAPKLSDLLKWVEETTPEDP
 ALAMTDHGNLFGAVEFYKKAEMGIEPILGTRPYVAAESP
 FDRKRKGGLDGGYFHLTLLAKDFTGYQNLVRLASRAYLEG 120
 FYEKPRIDREILRERRGPHRLSGCLGAEIPQFILQDRLDL
FFIEIQNHGLSEQK
 AEARLNEDLSIFKDRFFIHIQNHGLPEQKKVNEVLKEFAR
 KYGLGMVATNDGHYGRKEARSAHEVFLAIQSKSTLDDPGA 240
 VGFPLREFYVKTPEETCGPVFPPEEWGDEPFDNTVEIARM
 CNVELPIGTRWSTRI PRFPLPEGPGTEAKYLMELTFKGPL
 RRYPDRIITEGFYREVFRLLGKLPPHGHGEALAEALQVER 360
 EAWERLMKSLPPFDRGPRSS

Figure 16

| | Start1 | Start2 | 3'-Exo I |
|----------|--|--------|--|
| T.th. | VERVVRTLLDGRFLLEEGVGLWEWRYPPFLEGEAVVVLDLETTGLAG-----LDEVIEVGLLRLEGG---RRLPF | | |
| D.rad. | | | PWPQDVVVFDLETTGFSPA-----SAAIVEIGAVRIVGGQIDETLKF |
| Bac.sub. | HGIKMIYGMEANLVDDGVPIAYNAAHRLLEEETVVVFDVETTGLSAV-----YDTIIELAAVKVKGGE--IIDKF | | |
| H.inf. | | | MINPNRQIVLDLTETTTGMNQLGAHYEGHCIIIEIGAVELINRR-YTGNNX |
| E.c. | | | MSTAITRQIVLDLTETTTGMNQIGAHSEGHKIIIEIGAVEVNNRR-LTGNNF |
| H.pyl. | NLEYLKACGLNFIETSENLITLKNLKTPLKDEVF SFIDLETTG SCPI-----KHEILEIGAVQVKGGE--IINRF | | |

| | | 3'-Exo II |
|----------|---|-----------|
| T.th. | QSLVR-PLPP---AEARSWNLT---GIPREALEEAPSLEEVLKAYPLRGDATLV IHNAAFDLGFL -RPALEGLG | |
| D.rad. | ETLVR-PTRPDGSMLSIPWQAQRVHGISEMVRRAPAXKDVLPDFDFVDGSAVV AHNVSFDDGGFM -RAGAERLG | |
| Bac.sub. | EAFAN-PHRP---LSATIIELT---GITDDMLQDAPDVVDVIRDFREWIGDDILV AHNASFDMGFL -NVAYKKLL | |
| H.inf. | HIYIK-PDRP---XDPDAIKVH---GITDEMLADKPEFKEVAQDFLDYINGAELL IHNAFPDVGFM -DYEFRKLN | |
| E.c. | HVYLK-DRLV---DPEAFGVH---GIAVDFLLDKPTFAEVAVEFMDYIRGAELV IHNAAFDIGFM -DYEFSLLK | |
| H.pyl. | ETLVKVKVSP-----DYIAELT---GITYEDTLNAPS A HEALQELRLFLGNSVFV AHNAF D YNF LG RYFVEKLH | |

| | 3'-Exo IIIC |
|----------|---|
| T.th. | -----YRLNPVVDLSRLARRGLPGLRRYGLDALSEVLELPRRT-- CHRALED VERTLAVVHEVYYMLT-----SG |
| D.rad. | ----LSWAPERELCTMQLSRRAPFRERTHNLTVLAERLGLEFAPGGR HRSYGDVQVTAQAYLRLLLELLG -----ER |
| Bac.sub. | E---VEKAKNPVIDTLELGRFLYPEFKNHRLNTLCKKFDIELTQ-- HHRAIYDTE ATAYLLLKMLKDAA-----EK |
| H.inf. | -LNVKTDDICLVTDTLQMARQMPGKRN-NLDALCDRLGIDNSKRTL HGALLDAE ILADVYLMMTGGQTNLFD EE |
| E.c. | RDIAKTNTFCKVTDLSLAVARKMFPKGKRN-SLDALCARYEIDNSKRTL HGALLDAQ ILAEVYLAMTGGQTSMAFAME |
| H.pyl. | -----CPLLNLKLCTLDLSKRAILSMRY-SLSFLKELLGFGIEV-- SHRAYADAL ASYKLFEICLLNLP--SYIKT |

Figure 17

A)

ATGGTGGAGCGGGTGGTGCGGACCCCTTCTGGACGGGAGGT 40
 TCCTCCTGGAGGAGGGGTGGGGCTTTGGGAGTGGCGCTA
 CCCCTTTCCCTGGAGGGGGAGGCGGTGGTGGTCCTGGAC 120
 CTGGAGACCACGGGGCTTGCCGGCCTGGACGAGGTGATTG
 AGGTGGGCCTCCTCCGCCTGGAGGGGGGAGGCGCCTCCC 200
 CTTCCAGAGCCTCGTCCGGCCCCCTCCCGCCCGCCGAAGCC
 CGTTCGTGGAACCTCACCGGCATCCCCGGGAGGCCCTGG 280
 AGGAGGCCCTCCCTGGAGGAGGTTCTGGAGAAGGCCTA
 CCCCCTCCGCGGCGACGCCACCTTGGTGATCCACAACGCC 360
 GCCTTTGACCTGGGCTTCCTCCGCCCCGGCCTTGGAGGGCC
 TGGGCTACCGCCTGGAAAACCCCGTGGTGGACTCCCTGCG 440
 CTTGGCCAGACGGGGCTTACCAGGCCTTAGGCGCTACGGC
 CTGGACGCCCTCTCCGAGGTCTTGGAGCTTCCCCGAAGGA 520
 CCTGCCACCGGGCCCTCGAGGACGTGGAGCGCACCCCTCGC
 CGTGGTGACGAGGTATACTATATGCTTACGTCCGGCCGT 600
 CCCCACGCTTTGGGAACTCGGGAGGTAG

B)

MVERVVRTLLDGRFLLEEGVGLWEWRYPPFLEGEAVVVLD 40
 LETTGLAGLDEVIEVGLLRLEGGRRLPFQSLVRPLPPAEA
 RSWNLTGIPREALLEEAPSLEEVLKAYPLRGDATLVIHNA 120
 AFDLGFLRPALEGLGYRLENPVVDSLRLARRGLPGLRRYG
 LDALSEVLELPRRTCHRALEDVERTLAVVHEVYYMLTSGR 200
 PRTLWELGRZ

Figure 18

Alignment of dnaA genes.

| | | | | | | | |
|---------|-----------------|------------------|-----------------|------------------|------------------|------------------|-----|
| P.mar. | MLEASWEK | VQSSL--KQNLK-- | -----PSYE | TWIRPTEFSG--FKN | GELTLIAPNSFSSAW | LKNVYSQTIQETAE- | 65 |
| Syn.sp. | MVSCENLWQQ | ALAAIL--ATQLTK-- | -----PAFD | TIKASVLIS--LGD | GVATIQVENGFLVNH | LQKSYGPLIMEVLT- | 67 |
| B.sut. | MENILDLWNQ | ALAQI--EKKLSK-- | -----PSFE | TWMKSTKAHS--LQG | DTLTITAPNEFARDW | LESRYLHLIADTIY- | 67 |
| M.tub. | MTDDPGSGFTTVWNA | VVSELNGDPKVDGDP | SSDANLSAPLTPQOR | AWLNLVQPLT--IVE | GFALLSVPSSSFVQNE | IERHLRAPITDALS- | 87 |
| T.th. | MSHEAVWQH | VLEHI--RRSITE-- | -----VEFH | TWFERIRPLG--IRD | GVLELAVPTSFALDW | IRRHVAGLIQEGPR- | 66 |
| E.coli | MSLSLWQQ | CLARL--QDELP-- | -----TEFS | MWIRPLQAE--LSD | NTLALYAPNRFVLDW | VRDKYLNININGLLT- | 64 |
| T.mar. | MKER | ILQEI--KTRVNR-- | -----KSWE | LWFSSFDVKS--IEG | NKVVSFVGNLFKEW | LEKKYYSVLSKAVK- | 61 |
| H.pyl. | MDTNNNIEKE | ILALVKQNPVKVSL-- | -----IEYE | NYFSQLKYNPNASKS | DIAFFYAPNQVLCTT | ITAKYGALLKEILSQ | 72 |
| P.mar. | EIFG---EPVTVHVK | VKANAESSDEHYSSA | P----- | ---ITPPLEASPGSV | DSSGSSLRLSK---- | -KTLPLNLRVVFNR | 130 |
| Syn.sp. | DLTG---QEITVKLI | TDGLEPHS---LIGQ | E----- | ---SSLPMETTP--- | ----- | -KNATALNGKYTFSR | 115 |
| B.sut. | ELTG---EELSIKIV | IPQNQVEDFMPKPQ | VKKAVKEDTSDFPQN | ----- | ----- | -----MLNPKYTFDT | 119 |
| M.tub. | RRLGH-QIQLGVRIA | PGATDEADDTTVPPS | ENPATTSPDTTTDND | EIDDSAAARGDNQHS | WPSYFTERPHNTDSA | TAGVTSLNRRYTFDT | 176 |
| T.th. | LLGAQ-APRFELRVV | PGVVVQEDIFQPPPS | PPAQAP----- | ----- | ----- | -----EDTFKT | 108 |
| E.coli | SFCGADAPQLRFEVG | TKPVTQTPOAAVTSN | VAAPQAQVQTQPORA | APSTRSGWDNVPAPA | EP----- | -TYRSNVNVKHTFDN | 140 |
| T.mar. | VVLG---NDATFEIT | YEAPEPHSSYSEPLV | KKRAVLLTP----- | ----- | ----- | -----LNPDYTFEN | 106 |
| H.pyl. | NKVG-MHLAHSVDR | IEVAPKIQINAQSN | NYKAIKTS----- | ----- | ----- | -----VKDSYTFEN | 118 |
| P.mar. | FVVGPNRMAHAAAM | AVAESPGREFNPLFI | CGGVGLGKTHLMQAI | GHYRLEIDPGAKVSY | VSTETFTNDLIL--A | IRQDRMQAFDRDRYR- | 217 |
| Syn.sp. | FVVGPTNRMAHAASL | AVAESPGREFNPLFL | CGGVGLGKTHLMQAI | AHYRLEMPNPAKVY | VSTERFTNDLIT--A | IRQDNMEDFRSYR- | 202 |
| B.sut. | FVIGSGNRFABAASL | AVAEPAPAKAYNPLFI | YGGVGLGKTHLMHAI | GHYVIDHNPSAKVY | LSSEKFTNEFIN--S | IRDNKAVDFRNRYR- | 206 |
| M.tub. | FVIGASNRFAHAAAL | ATAEPARAYNPLFI | WGESGLGKTHLLHAA | GNYAQRFPGMRVKY | VSTEEFTNDFIN--S | LRDDRKVAFKRSYR- | 263 |
| T.th. | SWWGPTTPWPHGGAV | AVAESPGRAYNPLFI | YGGRGLGKTYLMHAV | GPLRAKRFPHMRLEY | VSTETFTNELINRPS | AR-DRMTEFREYR- | 196 |
| E.coli | FVEGKSNQLARAAAR | QVADNPGGAYNPLFL | YGGTGLGKTHLLHAV | GNGIMARKPNAKVY | MHSERFVQDMVK--A | LQNNAEIEFKRYR- | 227 |
| T.mar. | FVVGPGNSFAYHAAL | EVAKHPR-YNPLFI | YGGVGLGKTHLLQSI | GNVYVQNEPDLRVY | ITSEKFLNDLVD--S | MKEGKLNFEFREYR | 193 |
| H.pyl. | FVVGSCNNTVYEIAK | KVAQSDTPPYNPVLF | YGGTGLGKTHILNAI | GNHALEK--HKKVVL | VTSEDFLTDFLK--H | LDNKTMDSFKAHYR- | 203 |
| P.mar. | AADLILVDDIQFIEG | KEYTQEEFFHTFNAL | HDAGSQIVLASDRPP | SQIPRLQERLMSRFS | MGLIADVQAPDLETR | MAILQKKAHERVGL | 307 |
| Syn.sp. | SADFLILDDIQFIK | KEYTQEEFFHTFNAL | HEAGKQVVVASDRAP | QRIPGLQDRLLSRFS | MGLIADIQVPDLETR | MAILQKKAEDRIRL | 292 |
| B.sut. | NVDVLLIDDIQFIAG | KEQTQEEFFHTFNAL | HEESKQIVISSDRPP | KEIPTLEDRLRSRFE | WGLITDITPPDLETR | IAILRKKAKEGLDI | 296 |
| M.tub. | DVDVLLVDDIQFIEG | KEGQIEFFHTFNAL | HNANKQIVISSDRPP | QQLATLEDRLRTRFE | WGLITDVQPPELETR | IAILRKKAQMERLAV | 353 |
| T.th. | SVDLLLVDDVQFIAG | KERTQEEFFHTFNAL | YEAHKQIILSSDRPP | KDILTLEARLRSRFE | WGLITDNPAPDLETR | IAILKMNAS--SGPED | 285 |
| E.coli | SVDALLIDDIQFIAG | KERSQEEFFHTFNAL | LEGNQQIILTSDRYP | KEINGVEDRLKSRFG | WGLTVAIEPPELETR | VAIILMKKADENDIRL | 317 |
| T.mar. | KVDILLIDDVQFLIG | KTGVQTELFHTFNEL | HDSGKQIVICSDREP | QKLSEFQDRLVSRFQ | MGLVAKLEPPDEETR | KSIARKMLEIEHGEL | 283 |
| H.pyl. | HCDFLLDDAQFLQ | KPKLEEEFFHTFNEL | HANSKQIVLISDRSP | KNIAGLEDRLKSRFE | WGITAKVMPDLETK | LSIVKQKQCNQITL | 293 |
| P.mar. | PRDLIQFIAGRFTSN | IRELEGALTRAIFA | SITGLPMTVDSIAPM | LD----PNGQGEVET | PKQVLDKVAEVFKVT | PDEMRSASRRR-PVS | 392 |
| Syn.sp. | PKEVIEYIASHYTSN | IRELEGALIRAIAYT | SLSNVAMTVENIAPV | LN----PPVEKVAAA | PETIITIVAQHYQLK | VEELLSNSRRR-EVS | 377 |
| B.sut. | PNEVMYLIANQIDSN | IRELEGALIRVVAYS | SLINKDINADLAAEA | LKDII-PSSKPKVIT | IKETQRVVGGQFNK | LEDFKAKKRTK-SVA | 384 |
| M.tub. | PDDVLELIASSIERN | IRELEGALIRVTAF | SLNKTPIDKALAEIV | LRDLI-ADANTMQIS | AATIMAATAEYFDTT | VEELRGPGKTR-ALA | 441 |
| T.th. | PEDALEYIARQVTSN | IREWEGALMRASPTA | SLNGVELTRAVAACA | LRHLR-P--RELEAD | PLEIIRKAAGPVRPE | TPGGAGHERRRKEVV | 372 |
| E.coli | PGEVAFFIAKRLRSN | VRELEGALNRVIANA | NFTGRAITIDFVREA | LRDLL-A-LQEKLV | IDNIQKTVAEYKIK | VADLLSKRRSR-SVA | 404 |
| T.mar. | PEEVLFNFAENVDDN | LRRLRGAIKILVYK | ETTQGEVDLKEAILL | LKDFIKPNRVKAMP | IDELIEIVAKVTGVP | REEILSNRSNV-KAL | 372 |
| H.pyl. | PEEVMEYIAQHISDN | IRQMEGAIKISVNA | NLMNASIDLNLAKTV | LEDL--QKDHAEAGSS | LENILLAVAQSLNLK | SSEIKVSSRQK-NVA | 380 |
| P.mar. | QARQVGMVLMRQGTN | LSLPRIGDTFGGKDH | TTVMYAIEQVEKKLS | S-----DPQIA | SQVQKIRDLLQIDSR | RKR---- | 461 |
| Syn.sp. | LARQVGMVLMRQHTD | LSLPRIGAEFGGKDH | TTVMYSCDKITQLQQ | K-----DWETS | QTLTSLSHRINIAGQ | APES---- | 447 |
| B.sut. | FPRQIAMVLSREMTD | SSLPKIGEEFGGRDH | TTVIHAHEKISKLLA | D-----DEQLQ | QHVKEIKEQLK---- | ----- | 446 |
| M.tub. | QSRQIAMVLCRELTD | LSLPKIGQAFG-RDH | TTVMYAQRKILSEMA | E-----RREVF | DHVKEITRIRQRSK | R----- | 507 |
| T.th. | LPRQLAMVLRVLETP | ASLPEIGQLFGGRDH | TTVRYAIQKVQELAG | KP-----DREVQ | GLLRTLREACTDPVD | NLWITCG | 446 |
| E.coli | RPRQMAMALAKELTN | HSLPEIGDAFGGRDH | TTVLHACRKIEQLRE | E-----SHDIK | EDFSNLIRTLSS---- | ----- | 467 |
| T.mar. | TARRIGMYVAKNYLK | SSLRTIAEFKN-RSH | PVVVDSVKVKVDSLL | KG-----NKQLK | ALIDEVIGEISRRAL | SG----- | 440 |
| H.pyl. | LARKLVVYFARLYTP | NPTLSLAQFLDLKDH | SSISKMYSGVKMLE | EKSPFVLSLREBIK | NRLNELNDKKTAFNS | SE----- | 457 |

Figure 19

A)

GTGTGCGACGAGGCCGTCTGGCAACACGTTCTGGAGCACA
 TCCGCCGCAGCATCACCGAGGTGGAGTTCCACACCTGGTT
 TGAAAGGATCCGCCCTTGGGGATCCGGGACGGGGTGCTG 120
 GAGCTCGCCGTGCCACCTCCTTTGCCCTGGACTGGATCC
 GGCGCCACTACGCCGGCCTCATCCAGGAGGGCCCTCGGCT
 CCTCGGGGCCAGGCGCCCCGTTTGAGCTCCGGGTGGTG 240
 CCGGGGTCTGTAGTCCAGGAGGACATCTTCCAGCCCCCGC
 CGAGCCCCCGGCCAAGCTCAACCCGAAGATACCTTTAA
 AACTTCGTGGTGGGGCCCAACTCCATGGCCCCACGGC 360
 GGCGCCGTGGCCGTGGCCGAGTCCCCCGCCGGGCCTACA
 ACCCTCTCTCATCTACGGGGGCCGTGGCCTGGGAAAGAC
 CTACCTGATGCACGCCGTGGGCCCCACTCCGTGCGAAGCGC 480
 TTCCCCACATGAGATTAGAGTACGTTTCCACGGAACTT
 TCACCAACGAGCTCATCAACCGCCATCCGCGAGGGACCG
 GATGACGGAGTTCCGGGAGCGGTACCGCTCCGTGGACCTC 600
 CTGCTGGTGGACGACGTCCAGTTCATCGCCGAAAGGAGC
 GCACCCAGGAGGAGTTTTTCCACACCTTCAACGCCCTTTA
 CGAGGCCCAAGCAGATCATCCTCTCTCCGACCGGCCG 720
 CCCAAGGACATCCTCACCTTGAGGCGCGCCTGCGGAGCC
 GCTTTGAGTGGGGCCTGATCACCGACAATCCAGCCCCCGA
 CCTGGAAACCCGGATCGCCATCCTGAAGATGAACGCCAGC 840
 AGCGGGCCTGAGGATCCCGAGGACGCCCTGGAGTACATCG
 CCCGGCAGGTCACCTCCAACATCCGGGAGTGGGAAGGGC
 CCTCATGCGGGCATCGCCTTTCGCCTCCCTCAACGGCGTT 960
 GAGCTGACCCGCGCGGTGGCGGCCAAGGCTCTCCGACATC
 TTCGCCCCAGGGAGCTGGAGGCGGACCCCTTGAGATCAT
 CCGCAAAGCGGCGGACCAAGTTCGGCCTGAAACCCCGGGA 1080
 GGAGCTCACGGGGAGCGCCGCAAGAAGGAGGTGGTCTCTC
 CCGGCAGCTCGCCATGTACCTGGTGCGGGAGCTCACCCC
 GGCTCCCTGCCCGAGATCGACCAGCTCAACGACGACCGG 1200
 GACCACACCAGGTCTCTACGCCATCCAGAAGGTCCAGG
 AGCTCGCGAAAGCGACCGGGAGGTGCAGGGCCTCTCCG
 CACCTCCGGGAGGCGTGCACATGA

B)

VSHEAVQHVLEHIRRSITEVEFHTWFERIRPLGIRDGVL
 ELAVPTSFALDWIRRHAYAGLIQEGPRLGAQAPRFELRVV
 PGVVQEDIFQPPSPPAQAQPEDTFKTSWWGPTTPWPHG 120
 GAVAVAESPGRAYNPLFIYGGRLGKTYLMHAVGPLRAKR
 FPHMRLEYVSTETFTNELINRPSARDRMTEFRERYRSVDL
 LLVDDVQFIAGKERTQEEFFHTFNALYEAHKQIILSSDRP 240
 PKDILTLEARLSRFEWGLITDNPAPDLETRIAILKMNAS
 SGPEDPEDALEYIARQVTSNIREWEGALMRASPFASLNGV
 ELTRAFAAKALRHLRPRELEADPLEIRKAAGPVRPETPG 360
 GAHGERRKKEVVLPQQLAMYLVRLETPASLPEIDQLNDDR
 DHTTVLYAIQKVQELAESDREVQGLLRTLREACT

Figure 20

A)

ATGAACATAACGGTTCCCAAAAACTCCTCTCGGACCAGC 40
 TTTCCCTCCTGGAGCGCATCGTCCCCTCTAGAAGCGCCAA
 CCCCCTCTACACCTACCTGGGGCTTTACGCCGAGGAAGGG 120
 GCCTTGATCCTCTTCGGGACCAACGGGGAGGTGGACCTCG
 AGGTCCGCCTCCCCCGCCGAGGCCCAAAGCCTTCCCCGGGT 200
 GCTCGTCCCCGCCCAGCCCTTCTTCCAGCTGGTGCGGAGC
 CTCTCTGGGGACCTCGTGGCCCTCGGCCTCGCCTCGGAGC 280
 CGGGCCAGGGGGGGCAGCTGGAGCTCTCCTCCGGGCGTTT
 CCGCACCCGGCTCAGCCTGGCCCCCTGCCGAGGGCTACCCC 360
 GAGCTTCTGGTGCCCCGAGGGGGAGGACAAGGGGGCCTTCC
 CCCTCCGGACGCGGATGCCCTCCGGGGAGCTCGTCAAGGC 440
 CTTGACCCACGTGCGCTACGCCGCGAGCAACGAGGAGTAC
 CGGGCCATCTTCCGCGGGGTGCAGCTGGAGTTCTCCCCCC 520
 AGGGCTTCCGGGCGGTGGCCTCCGACGGGTACCGCCTCGC
 CCTCTACGACCTGCCCTGCCCAAGGGTTCCAGGCCAAG 600
 GCCGTGGTCCCCGCGGAGCGTGGACGAGATGGTGCGGG
 TCCTGAAGGGGGCGGACGGGGCCGAGGCCGTCTCGCCCT 680
 GGGCGAGGGGGTGTGGCCCTGGCCCTCGAGGGCGGAAGC
 GGGGTCCGGATGGCCCTCCGCCTCATGGAAGGGGAGTTCC 760
 CCGACTACCAGAGGGTCATCCCCAGGAGTTCCGCCCTCAA
 GGTCCAGGTGGAGGGGGAGGCCCTCAGGGAGGCGGTGCGC 840
 CGGGTGAGCGTCCTCTCCGACCGGCAGAACCACGGGTGG
 ACCTCCTTTTGGAGGAAGGCCGGATCCTCCTCTCCGCCGA 920
 GGGGGACTACGGCAAGGGGCAGGAGGAGGTGCCCCGCCAG
 GTGGAGGGGGCCGACATGGCCGTGGCCTACAACGCCCGCT 1000
 ACCTCCTCGAGGCCCTCGCCCCCGTGGGGGACCGGGGCCA
 CCTGGGCATCTCCGGGCCCCACGAGCCCGAGCCTCATCTGG 1080
 GGGGACGGGGAGGGGTACCGGGCGGTGGTGGTGGCCCTCA
 GGGTCTAG 1128

B)

MNITVPKLLSDQLSLLERIVPSRSANPLYTYLGLYAEEG 40
 ALILFGTNGEVDLEVRLPAEAQSLPRVLVPAQPPFQLVRS
 LPGDLVALGLASEPGQGQLELSSGRFRTRLAPAEGY 120
 ELLVPEGEDKGAFPLRTRMPSGELVKALTHVRYAASNEEY
 RAIFRGVQLEFSPQGFRAVASDGYRLALYDLPLPQGFQAK 200
 AVVPARSVDEMVRVLKGADGAEAVLALGEGVLALALEGGS
 GVRMALRLMEGEFPDYQRVIPQEFALKVQVEGEALREAVR 280
 RVSVLSDRQNHRVDLLLEGRILLSAEGDYGKGQEEVPAQ
 VEGPDMAYVAYNARYLLEALAPVGDRAHLGISGPTSPSLIW 360
 GDGEGYRAVVVPLRVZ

Figure 21

T.th.beta
E.coli.bet
P.mirab.be
H.infl.bet
P.put.beta
B.cap.beta

MNTVTPKKLLSDQSLLSLERIVPSRSANPLYTYLGLYAAEGALILFGTNGNEVDLEVRPAEY
MKFTVEREHLKPLQQVSGPLGGRPTLPILGNLLLQVADGTLSLTGTDLMEMVARVALV
MKFIIEREQLLKPLQQVSGPLGGRPTLPILGNLLKVTEINTLSLTGTDLMEMMARVSLS
MQFSISRENLLKLPLQQVCVLSNRPNIPVLNNVLLQIEDYRLTTGTDLLEVELSSQTQLS
MHFTIQREALLKPLQLVAGNVERQTLPVLNVVVGGQQLSTGTDLLEVELVGVRQLE
MKFTIQNDILTKNLKKITRVLVKNISFPPILENILIQVEDGTLSTTTNLEIELISKIEII
* . * * . . *

T.th.beta
E.coli.bet
P.mirab.be
H.infl.bet
P.put.beta
B.cap.beta

AQSLP-RVLVPAQPFFQLVRSPLPGDLVALGLASEPGQGQLELSSGRFRTRLSPAPAEY
QHPEPGATTVPARKFFDICRGLP-EGAEIAVQLE---GERMLVSRGRSRLSTLPAADF
QSHEIGATTVPARKFFDIWRGLP-EGAEISVELD---GDRLLVSRGRSRLSTLSPASDF
SSSENGTFTIPAKKFLDICRTLS-DDSEITVTFE---QDRALVQSGRSRFTLATQPAAEY
EPAPGEITVPARKLMDICKSLP-NDALIDIKVD---EQKLLVKAGRSRFTLSTLPANDF
TKYIPGKTTISGRKILNICRTLS-EKS KIMQLK---NKKMYISSSENSNYILSTLSADTF
. . . * . . . *

T.th.beta
E.coli.bet
P.mirab.be
H.infl.bet
P.put.beta
B.cap.beta

PELLVPEGEDKGAFPLRTRMPSEGELVKALTHVRYAASNEEYRAIFRGVQLEFSPQGFRVAV
PNLDD--WQSEVEFTLPQAT----MKRLIEATQFSMAHQDVRYLYNGMLFETEGEELRTV
PNLDD--WQSEVEFTLPQAT----LKRLIESTQFSMAHQDVRYLYNGMLFETENTEELRTV
PNLTD--WQSEVDFELPQNT----LRRLIEATQFSMANQDARYFLNGMKFETEGNLLRTV
PTVEE--GPSLTCNLQSK----LRRLIERTSFAMAQQDVRYLYNGMLLEVSRNTRLRAV
PNHQN--FDYISKFDISSNI-----LKEMIEKTEFSMGKDQDVRYLYNGMLLEKKDKFLRSV
* *

T.th.beta
E.coli.bet
P.mirab.be
H.infl.bet
P.put.beta
B.cap.beta

ASDG YRLALYDLPLPQGFQA--KAVVPARSVDEMVRVLKGADGAEAVLALGEGVLALALE
ATDGHRLAVCSMPIGQSLPS-HSVIVPRKGVIELMRMLDG-GDNPLRVQIGSNINRAHV
ATDGHRLAVCAMDIGQSLPG-HSVIVPRKGVIELMRLLDGSGESLLQLQIGSNINRAHV
ATDGHRLAVCTISLEQELQN-HSVILPRKGVLELVRLLET-NDEPARLQICTNNLRVHLK
STDGHRALCSCMSAPIEQEDRHQVIIVPRKGILELARLLTD-PEGMVSI VLGQHHIRATTG
ATDG YRLAISYTQLKKDINF-FSIIINPKAVMELLKLNT-QPQLLNILIGSNSIRIYTK
..** *** ..* *. .*

T.th.beta
E.coli.bet
P.mirab.be
H.infl.bet
P.put.beta
B.cap.beta

GGSGVRMALRLMEGEFFPDYQRVIPQEFAKLVQVEGEALREAVRRVSVLSDRQNHVRDLLL
---DFIFTSKLVDGRFPDYRRVLPKNPKDHLEAGCDLLKQAFARAAILSNEKFRGVRLYV
---DFIFTSKLVDGRFPDYRRVLPKNPKTKTVIAGCDILKQAFSRAAILSNEKFRGVRINL
---NTVFTSKLIDGRFPDYRRVLPARNATKIVEGNWEMLKQAFARASILSNERARSVRLSL
---EFTFTSKLVDGRFPDYERVLPKGGDKLVVGDRLREALFSAAILSNEKYRGIRLQL
---NLIFTTQLIEGEYPDYKSVLFKEKKNPIITNSILLKKSLLRVAILAHEKFCEGIEKI
. . . * . * . *

T.th.beta
E.coli.bet
P.mirab.be
H.infl.bet
P.put.beta
B.cap.beta

EGRILLSAEGDYGK-GQEEVPAQVEGPDMAVAYNARYLLEALAPVG-DRAHLGISGPTS
SENQLKITANNPEQEEAEIILDVITYSGAEMEIGFNVSYYLDVLNALKCENVRMMLTDSVS
TNGLQKITANNPEQEEAEIIVDVQYQGEEMEIGFNVSYYLDVLNLTCKCEEVKLLLTDAVS
KENQLKITASNTHEEEAEIIVDVYNAGEELEVGFNVTYILDVLNALKCNQVRMCLTDAFS
AAGQLKIQANNPEQEEAEIISVDYEGSSLEIGFNVSYYLDVLGVMTTEQVRMLILSDSNS
ENGKFKVLSDNQEEETAEDLFEIDYFGEKIEISINVYYLDVINNIKSENIALFLNKSKS
. . . . * . . *

T.th.beta
E.coli.bet
P.mirab.be
H.infl.bet
P.put.beta
B.cap.beta

PSLIWGDG-EGYRAVVVPLRVZ (ID#108)
SVQIEDAASQSAAYVVM PRLZ (ID#109)
SVQVENVASAAAAYVVM PRL- (ID#110)
SCIENCEDSSCEYVIMPRL- (ID#111)
SALLQEAGNDSSSYVVM PRL- (ID#112)
SIOIEAENNSSNAVVVMLKR- (ID#113)

Figure 22

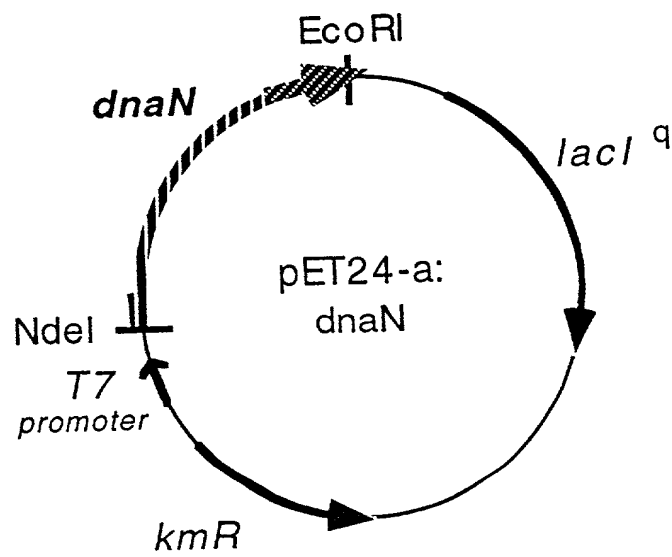
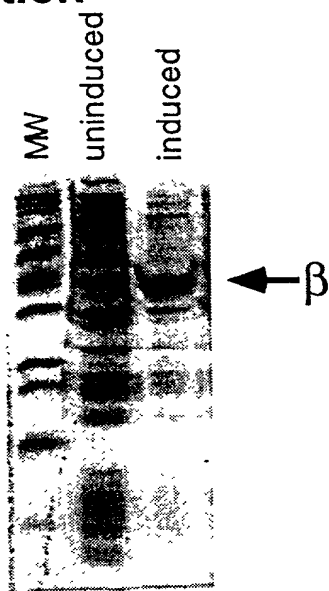


Figure 23

A) Induction

↓
Lysis

↓
Heat Step

B) MonoQ Column

Fraction: 5 7 9 11 13 15 17 19 21 23 25

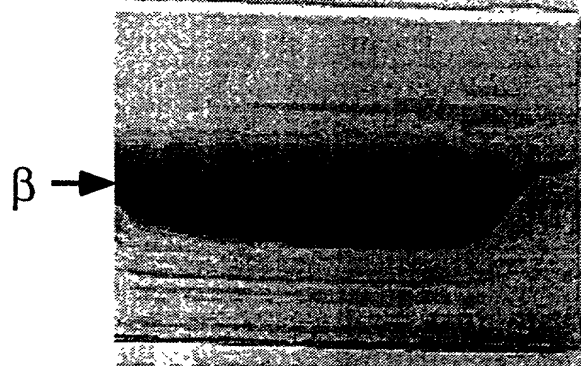


Figure 24

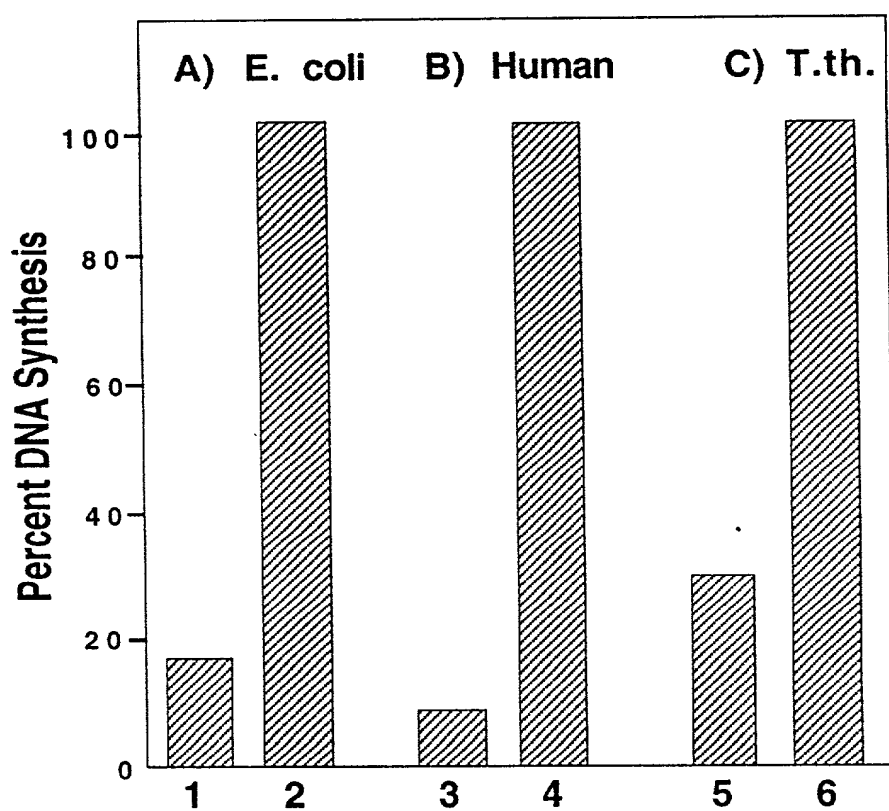
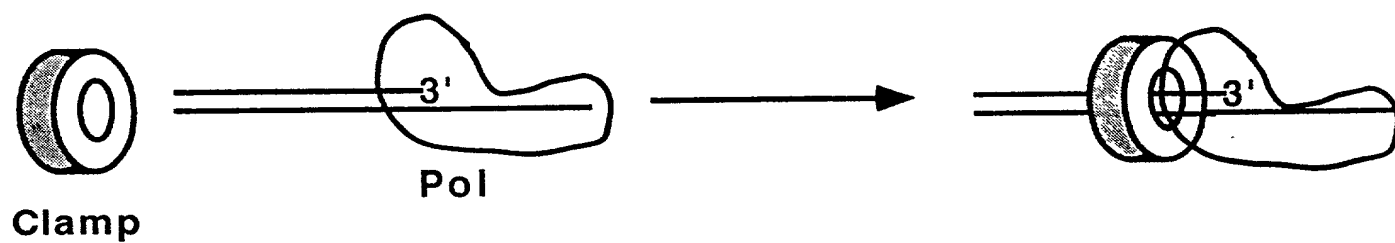


Figure 25

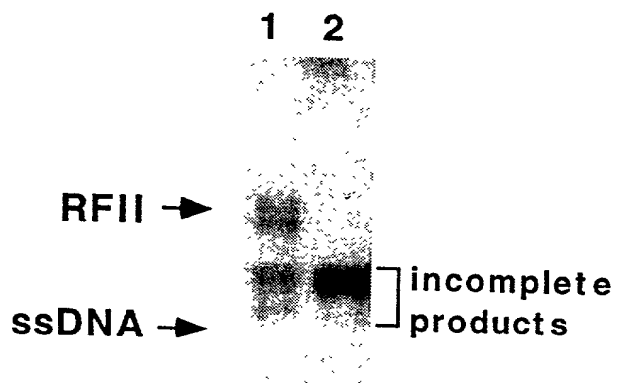
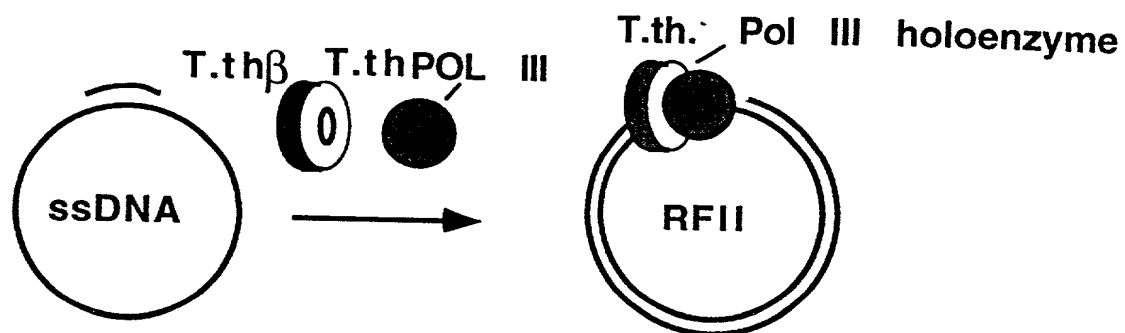


Figure 26